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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/437,458	11/10/1999	ANTHONY GIORDANO	50093/014001	8009

7590

08/23/2002

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176 FEDERAL STREET
BOSTON, MA 02110

EXAMINER

LEFFERS JR, GERALD G

ART UNIT	PAPER NUMBER
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1636

DATE MAILED: 08/23/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/437,458

Applicant(s)

GIORDANO ET AL.

Examiner

Gerry Leffers

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 04 June 2002.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 3 and 12-34 is/are pending in the application.
- 4a) Of the above claim(s) 12-27 and 29-31 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 3, 28 and 32-34 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
- If approved, corrected drawings are required in reply to this Office action.
- 12) ☒ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.
- 14) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☐ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____.
- 4) ☐ Interview Summary (PTO-413) Paper No(s). _____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: *detailed action/attach*.

DETAILED ACTION

Continued Prosecution Application

The request filed on 1/28/02 for a Continued Prosecution Application (CPA) under 37 CFR 1.53(d) based on parent Application No. 09/437,458 is acceptable and a CPA has been established. An action on the CPA follows.

Election/Restrictions

Applicant's election without traverse of Group 17 (claims 3, 28 and 32-34, drawn towards SEQ ID NO: 170 in Paper No. 22 is acknowledged. Claims 3 and 12-34 are pending in the instant application, with claims 12-27 and 29-31 withdrawn from consideration as drawn towards non-elected inventions.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:

Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c).

The information for Ashish Xavier has non-initialed alterations to the name.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

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Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title.

Claims 3, 28 and 32-34 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific (i.e. specific to the claimed invention) and substantial (i.e. that does not require further experimentation to establish a specific utility) asserted utility or a well established utility.

The rejected claims are directed towards an isolated fusion nucleic acid comprising a first nucleic acid (SEQ ID NO: 17) operably linked to a heterologous second nucleic acid and wherein the mRNA form of the first nucleic acids has RNA binding protein (RBP) binding activity or regulates the functionality of the mRNA form of the fusion nucleic acid. Hybrid transcripts comprising SEQ ID NO: 17 appear to be novel in the art. Therefore, there can be no well established utility for the claimed invention.

Asserted utilities for the claimed chimeric nucleic acids include 1) screening for compounds that affect the RBP binding activity of a particular RNA/RBP binding pair interaction, and/or the mRNA functionality; 2) to identify novel RNA/RBP binding pair interactions; and 3) to modify the expression of a protein encoded by the heterologous nucleic acid portion of the chimeric nucleic acid (e.g. page 10, first paragraph of the instant specification).

SEQ ID NO: 17 is disclosed in the instant specification as being obtained from the human leptin gene (Accession No. NM_000230). The specification generally describes an experiment where a protein extract from cells known to express leptin (3T3-L1) was used to demonstrate binding by an unidentified protein or proteins (RBPs) to an undescribed RNA comprising SEQ ID NO: 17 by either filter binding assay or gel filtration. While poly r(G), heparin and

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“unrelated” RNAs were used as non-specific inhibitors in the binding assays, the exact composition of the competing RNAs is not disclosed by the instant specification, making it unclear how specific the observed protein binding actually was for the RNA comprising SEQ ID NO: 17. Also, the actual binding/gel shift data is not provided by the instant specification, making it even harder to determine the specificity of the RBP/RNA interactions in this case. According to the information available at the NCBI web page for Accession No. NM_000230, the sequence represented by SEQ ID NO: 17 is present as a 3' untranslated region in the transcript encoding human leptin.

The asserted utilities are not specific in that the protein or proteins that apparently bound the RNA comprising SEQ ID NO: 17 are not identified in the instant specification. For example, using the claimed nucleic acid hybrid to identify compounds that affect a specific RNA/RBP binding pair cannot be considered to be a specific in the absence of an identified RBP specific to SEQ ID NO: 17. Moreover, the ability of the nucleic acid comprising SEQ ID NO: 17 to modify expression of a protein encoded by the fusion transcript in a specific manner (i.e. stabilize, destabilize, sequester, etc.) has not been demonstrated. Therefore, using the chimeric nucleic acid to modify the expression of a protein cannot be considered a specific utility. Finally, use of the claimed chimeric nucleic acid to identify novel RBP/RNA binding pairs cannot be considered specific because it is not known that the proteins that bound the RNA in the binding assay described in the specification do not also bind other RNAs (e.g. RNAs other than the unrelated RNAs used as non-specific inhibitors of binding).

The asserted utilities are not substantial in that for each of the asserted activities, it would require further experimentation in order to confirm a specific utility. For example, it would

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require further experimentation to determine the nature and number of different proteins responsible for binding the RNA comprising SEQ ID NO: 17 in the binding assay described in the specification. The asserted utility of using the chimeric nucleic acid to identify its own cognate binding proteins, if any, merely constitutes further experimentation to identify a specific activity.

Claims 3, 28 and 32-34 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 3, 28, 32-34 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The rejected claims are directed towards an isolated fusion nucleic acid comprising a first nucleic acid (SEQ ID NO: 17) operably linked to a heterologous second nucleic acid and wherein the mRNA form of the first nucleic acids has RNA binding protein (RBP) binding

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activity or regulates the functionality of the mRNA form of the fusion nucleic acid. Regulating functionality can comprise an alteration in pre-mRNA processing or in the stabilization, translational efficiency, localization, sequestration, editing or splicing functions. Thus, the rejected claims embrace a number of different possible effects of SEQ ID NO: 17 on a chimeric transcript comprising SEQ ID NO: 17.

SEQ ID NO: 17 is disclosed in the instant specification as being obtained from the human leptin gene (Accession No. NM_000230). The specification generally describes an experiment where a protein extract from cells known to express leptin (3T3-L1) was used to demonstrate binding by an unidentified protein or proteins (RBPs) to an undescribed RNA comprising SEQ ID NO: 17 by either filter binding assay or gel filtration. The context of SEQ ID NO: 17 in the total transcript was not described. While poly r(G), heparin and “unrelated” RNAs were used as non-specific inhibitors in the binding assays, the exact composition of the competing RNAs is not described by the instant specification, making it unclear how specific the observed protein binding actually was for the RNA comprising SEQ ID NO: 17. Also, the actual binding/gel shift data is not provided by the instant specification, making it even harder to determine the specificity of the RBP/RNA interactions in this case. There are no relevant working examples or data provided by the instant specification demonstrating the effect the presence of the sequence of SEQ ID NO: 17 on functionality of a transcript comprising SEQ ID NO: 17. No structural/functional basis is provided in the specification for one of skill in the art to envision what are the functional effects, if any, of SEQ ID NO: 17 on a transcript comprising SEQ ID NO: 17.

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According to the information available at the NCBI web page for Accession No. NM_000230, the sequence represented by SEQ ID NO: 17 is present as a 3' untranslated region in the transcript encoding human leptin. The prior art does not appear to disclose any embodiment wherein the sequence represented by SEQ ID NO: 17 has been used to modulate the functionality of any RNA, including its own. Therefore, the prior art does not offset the deficiencies of the instant specification as to the actual functional effects of SEQ ID NO: 17 on any transcript comprising the sequence.

Given that the claimed invention comprises a critical element of regulating mRNA functionality that embraces several different processes (e.g. stabilization, translational efficiency, etc.) and given the lack of a structural/functional basis in the instant specification or prior art to envision the actual effect of SEQ ID NO: 17 on a transcript comprising SEQ ID NO: 17, one of skill in the art would not be able to reliably envision the claimed invention. Therefore, one of skill in the art would reasonably conclude that applicants were not in possession of the claimed invention.

Response to Arguments

In response to a similar rejection under 35 U.S.C. 112, first paragraph, for lack of written description, applicants have submitted a declaration under 37 C.F.R. 1.132 from Dr. Anthony Giordano. The declaration by Dr. Giordano clearly teaches that the art recognizes that 5' and 3' UTRs can retain their RBP binding or regulatory activity when linked to heterologous coding sequences. However, the arguments presented by Dr. Giordano are moot as they do not address the current grounds of rejection. In the previous round of rejections, the basis for the rejection was the extremely broad genus of hybrid RNAs encompassed by the claims and the

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unpredictability as to whether the claimed UTR sequences would retain their functional activities in the context of a given hybrid transcript. In the current round of rejections, the basis for the rejection is a lack of description of the functional activity (i.e. stabilization, destabilization, translational efficiency, etc.) would be for those embodiments where the claimed UTR (i.e. comprising SEQ ID NO: 17) confers a means of regulating mRNA functionality for the hybrid comprising the claimed UTR. The declaration provided by Dr. Giordano does not address this point.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3 and 32-34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 3 and 32-34 are vague and indefinite in that is drawn towards non-elected embodiments (i.e. to SEQ ID NOS other than SEQ ID NO: 17). It would be remedial to amend the claim language to limit the embodiments to SEQ ID NO: 17.

A broad range or limitation together with a narrow range or limitation that falls within the broad range or limitation (in the same claim) is considered indefinite, since the resulting claim does not clearly set forth the metes and bounds of the patent protection desired. Note the explanation given by the Board of Patent Appeals and Interferences in *Ex parte Wu*, 10 USPQ2d 2031, 2033 (Bd. Pat. App. & Inter. 1989), as to where broad language is followed by "such as" and then narrow language. The Board stated that this can render a claim indefinite by

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raising a question or doubt as to whether the feature introduced by such language is (a) merely exemplary of the remainder of the claim, and therefore not required, or (b) a required feature of the claims. Note also, for example, the decisions of *Ex parte Steigewald*, 131 USPQ 74 (Bd. App. 1961); *Ex parte Hall*, 83 USPQ 38 (Bd. App. 1948); and *Ex parte Hasche*, 86 USPQ 481 (Bd. App. 1949). In the present instance, claim 33 recites the broad recitation "wherein the nucleic acid is DNA", and the claim also recites "cDNA" which is the narrower statement of the range/limitation. It would be remedial to amend the claims by creating two different dependent claims reciting the limitations of "DNA" or "cDNA".

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G Leffers Jr. whose telephone number is (703) 308-6232. The examiner can normally be reached on 9:30am-6:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (703) 305-1998. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 305-7939 for regular communications and (703) 305-7939 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

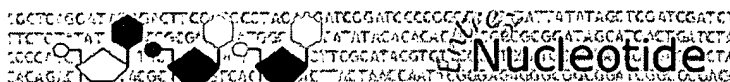
Gerald G Leffers Jr.
Examiner
Art Unit 1636

ggj
ggl

August 20, 2002

DAVID GUZO
PRIMARY EXAMINER





1: NM_000230. Homo sapiens
lept...[gi:4557714] MapView, Related Sequences, OMIM, Protein, PubMed, SNP, Taxonomy, UniSTS, LinkOut

8/19/02 8:32 PM

JOURNAL J. Biol. Chem. 271 (8), 3971-3974 (1996)
MEDLINE 96223958
PUBMED 8626726
REFERENCE 7 (bases 1 to 3426)
AUTHORS Niki T, Mori H, Tamori Y, Kishimoto-Hashimoto M, Ueno H, Araki S, Masugi J, Sawant N, Majithia HR, Rais N et al.
TITLE Human obese gene: molecular screening in Japanese and Asian Indian NIDDM patients associated with obesity
JOURNAL Diabetes 45 (5), 675-678 (1996)
MEDLINE 96198511
PUBMED 8621021
REFERENCE 8 (bases 1 to 3426)
AUTHORS Comuzzie, A.G., Hixson, J.E., Almasy, L., Mitchell, B.D., Mahaney, M.C., Dyer, T.D., Stern, M.P., MacCluer, J.W. and Blangero, J.
TITLE A major quantitative trait locus determining serum leptin levels and fat mass is located on human chromosome 2
JOURNAL Nat. Genet. 15 (3), 273-276 (1997)
MEDLINE 97207647
PUBMED 9054940
REFERENCE 9 (bases 1 to 3426)
AUTHORS Clement, K., Vaisse, C., Lahlou, N., Cabrol, S., Pelloux, V., Cassuto, D., Gourmelen, M., Dina, C., Chambaz, J., Lacorte, J.M., Basdevant, A., Bougneres, P., Lebouc, Y., Froguel, P. and Guy-Grand, B.
TITLE A mutation in the human leptin receptor gene causes obesity and pituitary dysfunction
JOURNAL Nature 392 (6674), 398-401 (1998)
MEDLINE 98196670
PUBMED 9537324
REFERENCE 10 (bases 1 to 3426)
AUTHORS Friedman, J.M. and Halaas, J.L.
TITLE Leptin and the regulation of body weight in mammals
JOURNAL Nature 395 (6704), 763-770 (1998)
MEDLINE 99010835
PUBMED 9796811

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [U43653.1](#).
Summary: This gene is similar to the mouse obesity gene (ob). The protein encoded by this gene is secreted by white adipocytes. In the mouse study, mutations in this gene are linked to severe and morbid obesity.

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Revised: July 5, 2002.

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Jul 16 2002 16:59:14

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31	7	(giordano-\$in. or xavier-\$in.) and utr	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:00
37	1	(giordano-\$in. or xavier-\$in.) and leptin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:01
43	206	leptin with (gene or rna or message or transcript or cdna)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:02
49	10	(leptin with (gene or rna or message or transcript or cdna)) with (fusion or chimera or hybrid)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:03

US-PAT-NO: 6258559

DOCUMENT-IDENTIFIER: US 6258559 B1

TITLE: Method for producing proteins in transformed *Pichia*

----- KWIC -----

In the following examples, *Pichia methanolica* strain PMAD16 was used as a host strain. This strain is derived from type strain CBS 6515 and is described by Raymond et al., *Yeast* 14:11 (1998), and by Raymond, "Recombinant Protein Expression in *Pichia methanolica*," in *Gene Expression Systems: Using Nature for the Art of Expression*, Fernandez and Hoeffler (eds.), pages 193-209 (Academic Press, Inc. 1999). The host strain carries both alcohol utilization genes *AUG1* and *AUG2* and is deleted for *PEP4* and *PRB1* proteases. For these studies, the *Pichia* contained an expression vector derived from pCZR1 34, which comprises an *AUG1* promoter, *AUG1* terminator, and *ADE2* as a selectable marker (Raymond et al., *Yeast* 14:11 (1998)). A chimeric gene comprising the following elements was inserted between the *AUG1* promoter and terminator: a *S. cerevisiae* *a-factor* prepro sequence, a Glu:Glu tag or a FLAG tag, and a human leptin gene. The human leptin gene has been described by Zhang et al., *Nature* 372:425 (1994). An illustrative method for constructing a plasmid that comprises a human leptin gene is described by Raymond et al., *BioTechniques* 26:134 (1999), and an exemplary human leptin amino acid sequence is provided by SEQ ID NO:7 (GenBank accession No. 4139908).

(FILE 'HOME' ENTERED AT 20:06:59 ON 19 AUG 2002)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 20:07:08 ON 19 AUG 2002

L1 13478 S (GIORDANO, ?)/IN,AU
L2 2724 S (XAVIER, ?)/IN,AU
L3 6 S L1 AND L2
L4 16196 S L1 OR L2
L5 16 S L4 AND LEPTIN
L6 0 S L4 AND (LEPTIN (S) UTR)
L7 3 S L4 AND (LEPTIN (S) (GENE OR RNA OR TRANSCRIPT OR MRNA))
L8 1 DUPLICATE REMOVE L7 (2 DUPLICATES REMOVED)
L9 13 S L5 NOT L7
L10 5 DUPLICATE REMOVE L9 (8 DUPLICATES REMOVED)
L11 50 S (FUSION OR CHIMER? OR HYBRID) (S) (LEPTIN (S) (GENE OR RNA
OR
L12 3 S L11 (S) REPORTER
L13 1 DUPLICATE REMOVE L12 (2 DUPLICATES REMOVED)
L14 25 DUPLICATE REMOVE L11 (25 DUPLICATES REMOVED)
L15 17531 S (GONG, ?)/IN,AU
L16 22 S L15 AND LEPTIN
L17 11 S L16 AND (LEPTIN (S) (GENE OR RNA OR TRANSCRIPT OR MRNA))
L18 3 DUPLICATE REMOVE L17 (8 DUPLICATES REMOVED)

From: Fredman, Jeffrey
Sent: Wednesday, June 12, 2002 3:00 PM
To: STIC-Biotech/ChemLib
Cc: Leffers, Gerald
Subject: FW: 09/437,458

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Leffers, Gerald
Sent: Wednesday, June 12, 2002 2:56 PM
To: Fredman, Jeffrey
Subject: 09/437,458

11A09
1636
11E12

Hi Jeff, please approve a RUSH search/interference search for this application for SEQ ID NO: 17 (~239 nucleotides).
Thanks, Gerry Leffers

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

Searcher: D. Schreber
Phone: 308-4292
Location: CM 6A03
Date Picked Up: 6/13
Date Completed: 6/14
Searcher Prep/Review: _____
Clerical: _____
Online time: 5

TYPE OF SEARCH:

NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): CompuLink

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:48 ; Search time 266.48 Seconds
(without alignments)
1539.862 Million cell updates/sec

Title: US-09-437-458-17

Perfect score: 239
Sequence: 1 cctggttcattcttactctgtg.....gtgagatcattcttactct.239

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Archived: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	239	22	AAH27148 Human leptin gene
2	239	100.0	3408	22	AAH27148 Human leptin (LEP)
3	239	100.0	3426	20	AAH27148 Human leptin (LEP)
4	239	100.0	4258	23	AAH27148 Human leptin (LEP)
5	80.6	33.7	2793	17	AAH27148 Human leptin (LEP)
6	80.6	33.7	2793	21	AAH27148 Human leptin (LEP)
7	80.6	33.7	2793	21	AAH27148 Human leptin (LEP)
8	80.6	33.7	2793	21	AAH27148 Human leptin (LEP)
9	80.6	33.7	2793	22	AAH27148 Human leptin (LEP)

10	73.4	30.7	5917	19	AAH27148 Human leptin gene	Porcine adipocyte
11	36	15.1	12237	24	AAH27148 Human leptin gene	Human immune system
12	35.8	15.0	5314	24	AAH27148 Human leptin gene	Human immune system
13	34.4	14.4	14861	24	AAH27148 Human leptin gene	Human immune system
14	34.4	14.4	14861	24	AAH27148 Human leptin gene	Human immune system
15	34.2	14.3	311	8	AAH27148 Human leptin gene	Human immune system
16	34.2	14.3	311	9	AAH27148 Human leptin gene	Human immune system
17	34.2	14.3	5551	11	AAH27148 Human leptin gene	Human immune system
18	34.2	14.3	5551	11	AAH27148 Human leptin gene	Human immune system
19	33.6	14.1	5449	24	AAH27148 Human leptin gene	Human immune system
20	33.6	14.1	13573	24	AAH27148 Human leptin gene	Human immune system
21	33.4	14.0	4116	20	AAH27148 Human leptin gene	Human immune system
22	33.3	13.8	8420	22	AAH27148 Human leptin gene	Human immune system
23	32.8	13.7	6392	24	AAH27148 Human leptin gene	Human immune system
24	32.8	13.7	6392	24	AAH27148 Human leptin gene	Human immune system
25	32.6	13.7	7119	24	AAH27148 Human leptin gene	Human immune system
26	32.6	13.6	16750	22	AAH27148 Human leptin gene	Human immune system
27	32.6	13.6	16750	24	AAH27148 Human leptin gene	Human immune system
28	32.2	13.5	5179	24	AAH27148 Human leptin gene	Human immune system
29	32.2	13.5	6040	24	AAH27148 Human leptin gene	Human immune system
30	31.8	13.3	440	22	AAH27148 Human leptin gene	Human immune system
31	31.8	13.3	440	22	AAH27148 Human leptin gene	Human immune system
32	31.8	13.3	5430	22	AAH27148 Human leptin gene	Human immune system
33	31.8	13.3	13125	24	AAH27148 Human leptin gene	Human immune system
34	31.8	13.3	13125	24	AAH27148 Human leptin gene	Human immune system
35	31.6	13.2	665	22	AAH27148 Human leptin gene	Human immune system
36	31.6	13.2	665	22	AAH27148 Human leptin gene	Human immune system
37	31.6	13.2	73334	24	AAH27148 Human leptin gene	Human immune system
38	31.4	13.1	6398	24	AAH27148 Human leptin gene	Human immune system
39	31.4	13.1	7384	24	AAH27148 Human leptin gene	Human immune system
40	31.4	13.1	15592	22	AAH27148 Human leptin gene	Human immune system
41	31.4	13.1	15592	22	AAH27148 Human leptin gene	Human immune system
42	31.4	13.1	15767	24	AAH27148 Human leptin gene	Human immune system
43	31.4	13.1	15767	24	AAH27148 Human leptin gene	Human immune system
44	31.2	13.1	6229	24	AAH27148 Human leptin gene	Human immune system
45	31.2	13.1	6568	24	AAH27148 Human leptin gene	Human immune system

ALIGNMENTS

RESULT 1	AAH27148	standard; DNA; 239 BP.
ID	AAH27148	standard; DNA; 239 BP.
AC	AAH27148	standard; DNA; 239 BP.
DT	08-AUG-2001	(first entry)
DE	Human leptin gene UTR region with RBP binding ability.	
XX	Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;	
KW	stroke; cardiovascular disease; hypertension; cancer; inflammation; ds;	
KW	leptin; metabolic disorder; obesity; diabetes.	
OS	Homo sapiens.	
PN	WO200134624-A1.	
XX	17-MAY-2001.	
PD	09-NOV-2000; 2000WO-US030888.	
PF	09-NOV-2000; 2000WO-US030888.	
XX	10-NOV-1999; 99US-0437458.	
PR	(MESS-) MESSAGE PHARM INC.	
PA	Giordano A, Xavier AK;	
PI	WPI; 2001-335904/35.	
DR	New nucleic acids that bind RNA-binding proteins or regulate mRNA	
XX	function, useful for therapeutic gene regulation, such as in cases of	
PT		

PT neurodegeneration -
 XX Claim 1: Page 30; 33pp; English.
 PS
 CC Sequences AAH27132 - AAH27151 represent human gene untranslated regions
 CC where the corresponding mRNA fragment has RNA binding protein (RBP)
 CC binding activity. RBPs mediate the processing of pre-mRNA, the transport
 CC of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
 CC translational efficiency, and the sequestration of some mRNAs. Therefore
 CC modification of post-transcriptional protein expression in eukaryotic
 CC cells may be carried out through the targeting specific interactions of
 CC proteins that bind to RBPs. The gene fragments of the invention are used
 CC to identify their optimized sub-fragments, compounds that interact with the
 CC interaction or mRNA functionality; or RBPs that interact with the
 CC compounds. Compounds identified using the gene fragments are potentially
 CC useful for therapeutic regulation of gene expression, such as in cases of
 CC neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
 CC inflammation; metabolic disorders (obesity and diabetes) and bacterial or
 CC viral infection. The present sequence is one of gene fragments of the
 CC invention, isolated from the human leptin gene.
 "v
 Sequence 239 BP: 54 A; 32 C; 68 G; 85 T; 0 other;
 Query Match 100.0%; Score 239; DB 22; Length 239;
 Best Local Similarity 100.0%; Pred. No. 6.4e-66;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ctggttcattctactctgtagtattacacacagtggttgcagtggttgcctg 60
 |||||||
 Db 1.ctggttcattctactctgtagtattacacacagtggttgcagtggttgcctg 60
 OY 61 agtgcattcccaagaccaggttatttaaaagattgtttgtcaagtgtcatatgta 120
 |||||||
 Db 61 agtgcattcccaagaccaggttatttaaaagattgtttgtcaagtgtcatatgta 120
 OY 121 ggtgtctgcacccagggtgtggaatgtttggcagaaggaagagatcagaatgtgt 180
 |||||||
 Db 121 ggtgtctgcacccagggtgtggaatgtttggcagaaggaagagatcagaatgtgt 180
 OY 181 ttcttgataacattgtgtggtgtcttcttggaagagtgagatctttctatct 239
 |||||||
 Db 181 ttcttgataacattgtgtggtgtcttcttggaagagtgagatctttctatct 239
 RESULT 2
 AAD17487
 ID AAD17487 standard; cDNA; 3408 BP.
 XX
 AAD17487;
 "f
 10-DEC-2001 (first entry)
 DE
 XX Human leptin (LEP) cDNA.
 XX
 KM Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;
 KM haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;
 KM beta-cell destruction; kidney tubule calcification; liver degeneration;
 KM diabetic retinopathy; cancer; coronary heart disease; growth disorder;
 KM dyslipidemia; coagulation disorder; stroke; peripheral vascular disease;
 KM hypertension; wasting syndrome; passive immunisation; immunosuppressive;
 KM Helicobacter pylori; arthritis; cardiovascular disease; ophthalmological;
 KM hypoglycaemic; anorectic; coagulant; cerebroprotective; antimicrobial;
 KM Leptin; LEP; vulnery; cytoskeletal; hypotensive; cardiant; human; ss.
 OS
 XX Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 40..543
 FT /*tag= a
 FT /product= "Human Leptin"
 XX
 PN MO200168828-A2.

XX 20-SEP-2001.
 PD
 XX
 XX 12-MAR-2001; 2001WO-1B00722.
 PF
 XX
 XX 13-MAR-2000; 2000US-0188796.
 PR
 XX 08-DEC-2000; 2000US-0254464.
 PA
 XX (ENGE-) ENGE INC.
 PI
 XX Kieffer TJ, Cheung AT;
 DR WPI: 2001-582445/65.
 DR P-PSDB: AAE10338.
 PT Novel isolated or cultured mucosal cell producing nutrient-regulatable
 PT protein expressed by transgene comprising expression control element
 PT linked with nucleic acid encoding protein, is useful for treating
 PT diabetes -
 PS
 XX Disclosure: Fig 17-18; 75pp; English.

The present invention relates to an isolated or cultured mucosal cell
 that produces a protein regulatable by a nutrient, where expression of
 the protein is conferred by a transgene comprising an expression control
 element in operable linkage with a nucleic acid encoding the protein.
 The invention is used in cell therapy and gene therapy. Isolated or
 cultured mucosal cell is useful for treating a hyperglycaemic condition
 such as type I diabetes (insulin-dependent diabetes), where the subject
 has a fasting plasma glucose level of greater than 110 mg/dl. It is also
 useful for treating obesity or undesirable body mass. Preferably, in
 these conditions the mucosal cell expresses insulin, leptin, glucagon-
 like peptide (GLP)-1, GLP-2, cholecystokinin (CCK), a glucagon
 antagonist, a growth hormone, a clotting factor or an antibody. The
 mucosal cells are implanted into a mucosal tissue or non-mucosal tissue
 such as liver, pancreas or muscle. Mice strains that develop or are
 susceptible to developing a particular disease (e.g. diabetes, cancer,
 degenerative disorders etc.) are also useful for introducing therapeutic
 proteins in order to study the effect of therapeutic protein expression
 in the disease susceptible mouse. Mucosal cell is also useful for
 treating insulin-independent (type 2) diabetes, degeneration of pancreas
 (beta-cell destruction), kidney tubule calcification, degeneration of
 liver, eye damage (diabetic retinopathy), diabetic foot, ulcerations in
 mucosa such as mouth and gums, excess bleeding, wound healing or delayed
 blood coagulation and increased risk of coronary heart disease, stroke,
 peripheral vascular disease, dyslipidemia, hypertension and obesity.
 Mucosal cell also produces protein such as clotting factors to treat
 haemophilia and other coagulation disorders, growth factors to treat
 growth disorders or wasting syndrome, and antibodies to provide passive
 immunisation or protection of a subject against foreign antigens or
 pathogens e.g. Helicobacter pylori or to provide treatment of cancer,
 arthritis, or cardiovascular disease. The present sequence is human
 leptin (LEP) cDNA.

Sequence 3408 BP; 880 A; 795 C; 911 G; 822 T; 0 other;

Query Match 100.0%; Score 239; DB 22; Length 3408;
 Best Local Similarity 100.0%; Pred. No. 1.6e-65;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ctggttcattctactctgtagtattacacacagtggttgcagtggttgcctg 60
 |||||||
 Db 1245 ctggttcattctactctgtagtattacacacagtggttgcagtggttgcctg 1304
 OY 61 agtgcattcccaagaccaggttatttaaaagattgtttgtaagtgatattgta 120
 |||||||
 Db 1305 agtgcattcccaagaccaggttatttaaaagattgtttgtaagtgatattgta 1364
 OY 121 ggtgtctgcacccagggtgtggaatgtttggcagaaggaagagatcagaatgtgt 180
 |||||||
 Db 1365 ggtgtctgcacccagggtgtggaatgtttggcagaaggaagagatcagaatgtgt 1424

OY 181 ttctcgaataacattcgtggtggtgttcttggaaagagtgagatcatttctatct 239
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1425 ttctcgaataacattcgtggtggtgttcttggaaagagtgagatcatttctatct 1483

RESULT 3

AAK59851
 ID AAK59851 standard; DNA; 3426 BP.

AC AAK59851;

DT 28-JUL-1999 (first entry)

DE SEQ ID 4 of WO9925824.

XX Mutation: human leptin; marker: obesity; hypogonadism;
 KM leptin secretion; leptin activity; ss.
 XX

XX Homo sapiens.

PN WO9925824-A1.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-FR02420.

XX 14-NOV-1997; 97FR-0014295.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Camoin L, Issad T, Ozata M, Strobel A, Strosberg AD;

DR WPI. 1999-338005/28.

XX Nucleic acid encoding a non-secreted human leptin mutant

XX Disclosure: Page 21-23; 31pp; French.

XX The specification describes a mutated human leptin that has Trp at
 CC position 105. The Arg105Trp mutation is a marker for subjects at risk
 CC of becoming obese, and for suitability of obese subjects for treatment
 CC with leptin. Subjects homozygous for the mutation are severely obese
 CC with hypogonadism, and have exceptionally low levels of leptin in the
 CC serum (the mutant is not secreted); heterozygotes are normal but
 CC carriers. Cells containing the mutated leptin cDNA sequence are used
 CC as model systems for studying mechanism of leptin secretion and
 CC activity, e.g. to differentiate between the reproductive and metabolic
 CC actions of leptin and to identify agents that affect specifically
 CC just one of these actions.

XX Sequence 3426 BP; 887 A; 798 C; 920 G; 821 T; 0 other;

XX Query Match 100.0%; Score 239; DB 20; Length 3426;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e-65;
 XX Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctggtttcatttctactgtgactgagtgttaccacagtggttgcacgtgttgcctg 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1262 ctggtttcatttctactgtgactgagtgttaccacagtggttgcacgtgttgcctg 1321
 OY 61 agtgaatcccaagcagcaggtattttaaagattgttttgcagtgcatatgta 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1322 agtgaatcccaagcagcaggtattttaaagattgttttgcagtgcatatgta 1381
 OY 121 ggtgttcacaccacaggggtggtggaatgtttggcagaagggagagatcagaatgtgt 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1382 ggtgttcacaccacaggggtggtggaatgtttggcagaagggagagatcagaatgtgt 1441
 OY 181 ttctcgaataacatttctgtgtgtgttcttcttggaaagagtgagatcatttctatct 239
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1442 ttctcgaataacatttctgtgtgtgttcttcttggaaagagtgagatcatttctatct 1500

RESULT 4

AAK78055
 ID AAK78055 standard; CDNA; 4258 BP.

AC AAK78055;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #13859.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX

OS Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI. 2001-639362/73.

DR P-PSDB; ABG13868.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 1; SEQ ID No 13859; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 4258 BP; 1109 A; 993 C; 1174 G; 982 T; 0 other;

XX Query Match 100.0%; Score 239; DB 23; Length 4258;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-65;
 XX Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctggtttcatttctactgtgactgagtgttaccacagtggttgcacgtgttgcctg 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1278 ctggtttcatttctactgtgactgagtgttaccacagtggttgcacgtgttgcctg 1337
 OY 61 agtgaatcccaagcagcaggtattttaaagattgttttgcagtgcatatgta 120

SQ Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;

1 ctggttcattctactgtgactgatatgttacatcacagtggttgcaatggtgttgcctg 60

AC AAF76943;

KW Murine; ob; leptin; antidiabetic; anorectic; anabolic;

OS Mus sp.
xy

PD 01-MAR-2001.

XX 23-ATG-1999. 99MS-1
PR

AA Banks WA;
PI

PT Modulator

PT modulating transport of leptin across the blood-brain barrier for
PT modulating body weight and appetite in a mammal, involves administering
PT adrenergic agonist or antagonist, neurotransmitter or cytokines -

CC The present sequence encodes murine leptin. It is given in a

AA	Sequence
50	2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other

QY 1 ctggttcatttctactgtgactgatgttaccatcacagtggttgcaatggtgtgacctg 60

AAV17090 AC

DE Porcine adipocyte polypeptide Leptin encoding DNA

OS	Sus scrofa
yy	

CDs
ET

ET

ET ET

PN WO9804690-A1
XX
PD 05-FEB-1998.

3 The present sequence encodes porcine adipocyte polypeptide leptin.
 CC Measuring levels of leptin, or the nucleic acid encoding it, in
 CC biological fluids or tissues is used to determine the susceptibility of
 CC pigs to deposit fat. Similar measurements done in vitro on adipocytes in
 CC presence of a test compound are used to identify agents that can
 CC modulate fat deposition. Excessive fat deposition in pigs can be
 CC prevented, and energy intake, metabolism and weight gain controlled by
 CC treatment with leptin, antibodies against it or nucleic acids encoding
 CC it. The same results are achieved by altering expression of the leptin-
 CC encoding gene. Host cells containing leptin encoding nucleic acids are
 CC used for production of recombinant leptin and its associated nucleic
 CC acids, or its fragments, can be used to isolate related sequences. Ab
 CC are also useful as immunoassay reagents for leptin or for affinity
 CC purification. Leptin can be administered by injection or orally
 CC (including consumption in genetically altered feeds). Use of leptin
 CC provides pigs with reduced levels of fat and allows matching of nutrient
 CC content of feed with nutritional requirements of the feed. The
 CC treatments can be applied to growing, finishing, lactating or pregnant
 CC pigs.

RESULT	11
ABL34358	
ID	ABL34358 standard; DNA; 12237 BP.
XX	
XX	
AC	ABL34358;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SPQ
XX	
ID	NO: 2331

Query Match	15.1%	Score 36;	DB 24;	Length 12237;
Best Local Similarity	51.9%	Pred. NO. 0.41;		
Matches	81;	Conservative	0;	Mismatches 75; Indels 0; Gaps 0;
Oy	80	ggtatttttaaagaagatttgcctttgttcaagatgctacatgtatgagtgtctgcaccacggggt	139	
Db	5847	ggctttttttaaagaagtaatgttttttttgcataaaagtggtatatattattttaagcgggt	5906	
Oy	140	ggggaaatgcttttggcgcagaagggagaagatctagaatgtgtttctgataacatttgcg	199	
Db	5907	ggatagatgttaagtttggggtttggggaagcttttgggatacatatgttagtttgttatctt	5966	
Oy	200	tgtgtggtctcttcttggaaagatgagatcatcttctc	235	
Db	5967	gggttgggttgagtcgaagaaagtgctttattctttc	6002	

RESULT	12
ABL32161	
ID	ABL32161 standard; DNA; 5314 BP.
XX	
XX	
AC	ABL32161;
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 134.
XX	
XX	
KW	Human; immune system disease; cytosine methylation; antiasthmatic; antiasthmatic; antileukemic; antianeumatic; cytoskeletal; neotropic; antiasthmatic; antileukemic; antianeumatic; cytoskeletal; neotropic;

KM Human; immune system disease; cytosine methylation; antiasthmatic;
KM antiarteriosclerotic; antiandemic; cytostatic; nootropic;
KM neuroprotective; anti-HIV; anticonvulsant; pathomorphological;
KM antileukemic; antiarthritic; antidiabetic; antisorbic;
KM antirheumatic; antiaortic; antiparasitic; antiparasitic;

KW Human; gene regulation-associated gene; severe combined immunodeficiency
 KW cardiac damage; inflammatory response; Hemophilia; Werner syndrome;
 KW ashlma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
 renal disease; Preeclampsia; cardiac allograft vascular disease;
 KW colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
 KW immunostimulant; cardiac; antiinflammatory; coagulant; antistatic;
 KW

nephrotropic; gynecological; anti-tumour; immunosuppressive; cytosolic.

OS Homo sapiens.
PN MO200177375-A2.
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-EP03968.
XX
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1033529.
PR 01-SEP-2000; 2000DE-1043826.
PA (EPIC-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;

WIPI: 2002-017470/02.
XX
XX
PT New nucleic acid sequences from chemically modified genes associated
PT with gene regulation, useful for analysing cytosine methylations for
PT diagnosis and therapy of diseases e.g. severe combined immunodeficiency
PT disease
XX
PS Claim 1: SEQ ID NO 162; 26pp; English.
XX
XX The invention relates to 224 nucleic acid sequences comprising at least
CC 18 bases of a chemically pretreated gene associated with gene regulation
CC selected from 43 known genes (or complementary sequences). The
CC chemical pretreatment converts cytosine bases unmethylated at the
CC 5'-position to uracil or another base with hybridisation behaviour
CC dissimilar to cytosine, to enable analysis of cytosine methylations.
CC The DNA sequences, oligomers (or sets/arrays) and method are
CC useful in the diagnosis of diseases (or predisposition to diseases)
CC associated with gene regulation and in therapy of such diseases, by
CC enabling analysis of the cytosine methylation patterns of such genes,
CC kits are provided. They are especially useful in diagnosis
CC and therapy of e.g. severe combined immunodeficiency disease, cardiac
CC disorders, haemophilia, solid tumours and cancer, Werner syndrome,
CC asthma, HHR syndrome, Saelene-Choitzen syndrome, renal disease,
CC preclampsia, graft versus-host disease. The present sequence is a
CC sequence included in the sequence data for this specification and is
CC associated with the human gene regulation-associated genes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 14861 BP; 3658 A; 228 C; 4018 G; 6955 T; 2 other;

Query Match 14.4%; Score 34.4; DB 24; Length 14861;
Best Local Similarity 51.3%; Pred. No. 1.4;
Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

OY 82 ttattttaaagaattgtttcgaagtgcatatgtagtgcgtccaccagggtgg 141
| | | | | | | | | | | | | | | | | | | |
Db 6918 ttatttcattgatatttatagtaaatggtcaatatgctcggtttaagggtgtgtgga 6977

OY 142 ggaatgtttggcagaagggaaagagatcagaatgagtgtttctgatacacatttgtg 201
| | | | | | | | | | | | | | | | | | | |
Db 6978 ggaaggttaggaaaaagggaggaggaagttagttattctgttgagtgatttgttg 7037

OY 202 gtgggtctcttggaaaggagtgagatcatttcttat 237
| | | | | | | | | | | | | | | | | | | |
Db 7038 gggtgtgtttttttatttagaaaatgtttttaatlt 7073

RESULT 15
AAAT0097
ID AAAT0097 standard: DNA; 311 BP.

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:48 ; Search time 75.79 Seconds
(without alignments)
774.593 Million cell updates/sec

Title: US-09-437-458-17

Perfect score: 239
Sequence: 1 cgtgattcattctactctgtyg.....gtgagatcattcttctatct 239

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

arched: 383533 segs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCITUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	239	100.0	239	4	US-09-437-457-17 Sequence 1, Appl
2	80.6	33.7	2793	2	US-08-347-563A-1 Sequence 1, Appl
3	80.6	33.7	2793	3	US-08-485-942A-1 Sequence 1, Appl
4	80.6	33.7	2793	3	US-08-488-214A-1 Sequence 1, Appl
5	80.6	33.7	2793	3	US-08-488-208A-1 Sequence 1, Appl
6	80.6	33.7	2793	4	US-08-488-211A-1 Sequence 1, Appl
7	80.6	33.7	2793	4	US-08-488-223A-1 Sequence 1, Appl
8	73.4	30.7	5917	4	US-08-692-922-1 Sequence 1, Appl
9	29.8	12.5	2449	4	US-08-840-767-7 Sequence 1, Appl
10	29	12.1	5474	1	US-08-137-252-2 Sequence 1, Appl
11	28	11.7	3111	2	US-09-014-969-12 Sequence 12, Appl
12	27.8	11.6	824	2	US-08-922-170B-12 Sequence 12, Appl
13	27.8	11.6	3098	1	US-08-447-500-1 Sequence 1, Appl
14	27.8	11.6	3098	1	US-08-454-097-1 Sequence 1, Appl
15	27.8	11.6	3098	1	US-08-447-408-1 Sequence 1, Appl
16	27.8	11.6	3098	1	US-08-453-866-1 Sequence 1, Appl
17	27.8	11.6	3098	1	US-08-185-359-1 Sequence 1, Appl
18	27.6	11.5	1380	4	US-09-181-336-16 Sequence 16, Appl
19	27.4	11.5	90050	4	US-09-245-041-5 Sequence 5, Appl
20	27.2	11.4	5051	2	US-08-239-276-2 Sequence 2, Appl
21	27.2	11.4	5051	2	US-08-468-579B-2 Sequence 2, Appl
22	27.2	11.4	5051	3	US-08-468-577B-2 Sequence 2, Appl
23	27.2	11.4	12720	1	US-08-403-866-11 Sequence 11, Appl
24	27	11.3	2508	4	US-09-347-833-1 Sequence 1, Appl
25	27	11.3	8600	4	US-09-457-708-1 Sequence 1, Appl
26	26.8	11.2	1693	6	US-09-328-111-626 Sequence 626, App
27	26.6	11.1	935	4	US-09-328-111-626 Sequence 626, App

28	26.6	11.1	946	3	US-09-188-930-258 Sequence 258, App
29	26.6	11.1	2328	1	US-08-688-649-38 Sequence 38, Appl
30	26.6	11.1	2328	4	US-09-715-524B-1 Sequence 1, Appl
31	26.6	11.1	3499	1	US-07-966-278-2 Sequence 2, Appl
32	26.6	11.1	3499	1	US-08-424-921-2 Sequence 2, Appl
33	26.6	11.1	3499	2	US-08-556-355A-2 Sequence 2, Appl
34	26.6	11.1	3499	2	US-07-803-627A-2 Sequence 2, Appl
35	26.6	11.1	4823	2	US-08-457-254-5 Sequence 5, Appl
36	26.6	11.1	4823	2	US-08-484-257-20 Sequence 20, Appl
37	26.6	11.1	4823	3	US-08-999-927-5 Sequence 5, Appl
38	26.6	11.1	4823	4	US-08-461-819-5 Sequence 5, Appl
39	26.6	11.1	4823	5	PCT-US94-08806-28 Sequence 28, Appl
40	26.6	11.1	4823	5	PCT-US95-01829-5 Sequence 5, Appl
41	26.6	11.1	4823	5	PCT-US95-01829-5 Sequence 5, Appl
42	26.4	11.0	1728	2	US-08-417-495-1 Sequence 1, Appl
43	26.4	11.0	1728	2	US-08-284-391B-1 Sequence 1, Appl
44	26.4	11.0	1728	4	US-09-218-950-1 Sequence 1, Appl
45	26.4	11.0	1728	5	PCT-US92-01785-1 Sequence 1, Appl

ALIGNMENTS

```
RESULT 1
US-09-437-457-17
Sequence 17, Application US/09437457
Patent No. 6273893
GENERAL INFORMATION:
APPLICANT: Giordano, Anthony
APPLICANT: Xavier, Ashish
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
FILE REFERENCE: 50093/014001
CURRENT APPLICATION NUMBER: US/09/437,457
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 17
LENGTH: 239
TYPE: DNA
ORGANISM: Homo sapiens
US-09-437-457-17

Query Match 100.0%; Score 239; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.6e-69;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgtgttctattctactctgtgactgattacacagtggttgcagtgtgttgcctg 60
DB 1 cgtgttctattctactctgtgactgattacacagtggttgcagtgtgttgcctg 60
QY 61 agtgcattcccaagcagcaggtattttaaaagatttcttgcagtgatcata 120
DB 61 agtgcattcccaagcagcaggtattttaaaagatttcttgcagtgatcata 120
QY 121 ggtgtctgcaccaggggtggggaatgttggcagaaggaggaagatcagaatgct 180
DB 121 ggtgtctgcaccaggggtggggaatgttggcagaaggaggaagatcagaatgct 180
QY 181 ttctgcaataattgtgtgtgttcttgggaaggagtgagatcttctatct 239
DB 181 ttctgcaataattgtgtgtgttcttgggaaggagtgagatcttctatct 239

RESULT 2
US-08-347-563A-1
Sequence 1, Application US/08347563A
Patent No. 5935810
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
```

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GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAS, KETAN GAUJWALA, AND STEPHEN K. BI
TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
TITLE OF INVENTION: AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,942A
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6048837ember 30, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Murine ob cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Murine
FEATURE:
NAME/KEY: CDS
LOCATION: 57..560
US-08-485-942A-1
Query Match 33.7%, Score 80.6; DB 3; Length 2793;
Best Local Similarity 65.4%; Pred. No. 4e-17;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
Oy 1 ctgtgttaattctactctgtgactgctgttacttcacagtggttgaagtggtgcctg 60
||||| |||||| ||||||| || | ||||||| || |||||
Db 1225 CTGGTTGGTTCATATGCTGACCTCATCCAAACAGCTTGCGAGCGGCAATGCC--- 1281
Oy 61 agtgcattcccaagcagcaggttatttcaaaagaattggttgcacagtgcatatgta 120
||||| |||| | |||| | ||||| ||||||| |||||||
Db 1282 --GGAGCATAGAGCGATAGTATTATCAAAAGCAGATGATTTTGCAAGTGTAATATGTA 1339
Oy 121 gggtgtctgcaccacaggggtgggaatggttgggcagaagggagaagatctagaatgtct 180

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33.7%; Score 80.6; DB 3; Length 2793;

STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Murine ob cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Murine
FEATURE:
NAME/KEY: CDS
LOCATION: 57..560
US-08-488-208A-1

Query Match 33.7%; Score 80.6; DB 3; Length 2793;
Best Local Similarity 65.4%; Pred. No. 4e-17;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

QY 1 ctggttcattctactgactgactgtatcatcacagtggttgcacatggtggtccctg 60
DB 1225 CTGCTTTGTTCTATTGTGACTGACTCTATCCAAACACGTTTGACGGCATGGCC--- 1281
61 agtgcattcccaagcagcaggtattttaaagattgttttgcagtgcatatgta 120
DB 1282 --GGGACCATAGGCTAGCTATATATCAAAAGCATGATTTTGTCAAGTGAATATGTA 1339
QY 121 ggtgtctgcaccaggggtggtggaatgttgcgcagaagaggaagatctagaatgtgt 180
DB 1340 TCTATGTGCACTGAGGCTAGAGGATGTGTAGAGGAGGCTGAAGATCCGGAA-GTGT 1398
QY 181 ttctgataacattgtgtgtgtgtgttcttggaaagagtgagatcatt 231
DB 1399 TCTCTGATTAACATATGTGTGTAGGCTTTCTGAAAGGCTGAGGCATTTT 1449

RESULT 6

US-08-483-211A-1
Sequence 1, Application US/08483211A
Patent No. 6309833

GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,211A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6309853ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5600
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Murine ob cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Murine
FEATURE:
NAME/KEY: CDS
LOCATION: 57..560
US-08-483-211A-1

Query Match 33.7%; Score 80.6; DB 4; Length 2793;
Best Local Similarity 65.4%; Pred. No. 4e-17;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

QY 1 ctggttcattctactgactgactgtatcatcacagtggttgcacatggtggtccctg 60
DB 1225 CTGCTTTGTTCTATTGTGACTGACTCTATCCAAACACGTTTGACGGCATGGCC--- 1281
QY 61 agtgcattcccaagcagcaggtattttaaagattgttttgcagtgcatatgta 120
DB 1282 --GGGACCATAGGCTAGCTATATATCAAAAGCATGATTTTGTCAAGTGAATATGTA 1339
QY 121 ggtgtctgcaccaggggtggtggaatgttgcgcagaagaggaagatctagaatgtgt 180
DB 1340 TCTATGTGCACTGAGGCTAGAGGATGTGTAGAGGAGGCTGAAGATCCGGAA-GTGT 1398
QY 181 ttctgataacattgtgtgtgtgtgttcttggaaagagtgagatcatt 231
DB 1399 TCTCTGATTAACATATGTGTGTAGGCTTTCTGAAAGGCTGAGGCATTTT 1449

RESULT 7

US-08-488-223A-1
Sequence 1, Application US/08488223A
Patent No. 6350730

GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: <Unknown>


```

TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-12

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Query Match 11.7%; Score 28; DB 2; Length 3111;
Best Local Similarity 49.3%; Pred. No. 7.6;
Matches 73; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 72 aagacccaggtatatttaaaagattttgtcagtgatcatatgtgtgtcgcac 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2636 ATGGAACGCTGATTTATACATTTAAGATGCTCTTTGCTTTAACTGCAT 2695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 132 ccaggggtgggaatgtttggcagaaggaagatcagaatgttttcgaataa 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2696 GCTGCCAAGTGCATTTGGGTCACATCCGTTTCAACACAGTGTCTCTGTTAT 2755
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    192 cattgtgtgtgtgttttttggaaaga 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    2756 CATGTGAACGTGGGTTCTGTTACGA 2783

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```

RESULT 12
US-08-922-1708-12
Sequence 12, Application US/08922170B
Patent No. 5968822
GENERAL INFORMATION:
APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
APPLICANT: Feinstein
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Robert Shelnbein
STREET: 2940 Birchtree Lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890PX
OPERATING SYSTEM: MS DOS version 6.2,

```

```

OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
SOFTWARE: an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,170B
FILING DATE: 2 SEP 1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 910/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 824
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-922-1708-12

```

```

Query Match 11.6%; Score 27.8; DB 2; Length 824;
Best Local Similarity 47.4%; Pred. No. 5.2;
Matches 83; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 9 attctactgtgactgcatgcatcacacagtggttgcagtgttccctgaatgac 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 603 AATGCCAAATTCCTGCTGTATATGAATAAAGCATACGTTACCCCTGACACAAA 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 69 tccaagacacaggtatttaaaagattgtttgtcagtgcatatgtagtgc 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 663 GCCGAGGGGGGCTTTATTCATAAACAACCCATGTTAGAGGCCACCTCTGCCGA 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 129 caccaggggtgggaatgtttggcagaaggaagatcagaatgtttt 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 723 GTTCCAGAGCTTCGGAGGGGTACACTCATGATTTACATTCACGTGTGTGT 777
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```

```

RESULT 13
US-08-447-500-1/c
Sequence 1, Application US/08447500
Patent No. 5627064
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,500
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/008,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.

```



```

? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? IMMEDIATE SOURCE:
? CLONE: Tyrosine Kinase
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 879..2364
?
US-08-447-408-1

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Query Match	11.6%	Score 27.8	DB 1	Length 3098
Best Local Similarity	50.4%	Pred. No. 8.9		
Matches 68	Conservative 0	Mismatches 67	Indels 0	Gaps 0

Qy	83	tattctaaagaatcttcttgcaagtcatgtaggtgcctgaccagggytgg	142
	361	TCTTTTAATTATFANCCTTATTACGCAGGCCGTRTCGAGGACAATACCGAATGGTTTAG	302
Qy	143	gaatcgttcggcaggaagsgaagaatctaagaatgctttccgaataacatlttgtg	202
Dd	301	ATCTTTTAGTATACAAATTAAGCGAGATATAAATGGTGTTGTGATGTTACTAGTGTTA	242
Qy	203	tgggtctcttgaag	217
Dd	241	TTGATTAATAAGAAG	227

Search completed: June 13, 2002, 15:19:07
Job time: 8959 sec

Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctggttcattctactgtagctgacgtatgacacacagtggttgcattggtgacctg 60
 |||||
 DB 1 CTGTTTCAATTTCTACTGCTGACTGATGTACATCACAGTGTTCGAATGCTGCCCTG 60

QY 61 agtgcattcccaagaccaggtttttaaaagattgtttgtcgaagtgcatactgta 120
 |||||
 DB 61 AGTGCATCTCCAGACAGGCTTATTTTAAAAAGATTGTTTGTCAAGTGTCAATGTGA 120

QY 121 ggtctgcaccacagggtggtggaatgttctgacagaaggagaagatctagaatgtgt 180
 |||||
 DB 121 GGTCTGTGACACCCAGGCTGGGGAATGTTTGGCGCAAGAGGAGATCTTGAAATGTCT 180

QY 181 ttctcgaataacattgt 239
 |||||
 DB 181 TTCTCGAATAACATTTGT 239

RESULT 2
 ...03702
 US AX003702 3426 bp DNA linear PAT 24-AUG-2000
 .JINITION Sequence 4 from Patent WO9925824.
 ACCESSION AX003702
 VERSION AX003702.1 GI:9927488
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 3426)
 AUTHORS Issad,T. and Camoin,L.
 TITLE Cdna sequence coding for a mutated leptin and applications
 JOURNAL Patent: WO 9925824-A 4 27-MAY-1999;
 ISSAD TARIK (FR); CAMOIN LUC (FR)
 FEATURES location/Qualifiers
 source 1..3426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 887 a 798 c 920 g 821 t

ORIGIN

Query Match 100.0%; Score 239; DB 6; Length 3426;
 Best Local Similarity 100.0%; Pred. No. 5.1e-62;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctggttcattctactgtagctgacgtatgacacacagtggttgcattggtgacctg 60
 |||||
 DB 1262 CTGTTTCAATTTCTACTGCTGACTGATGTACATCACAGTGTTCGAATGCTGCCCTG 1321

QY 61 agtgcattcccaagaccaggtttttaaaagattgtttgtcgaagtgcatactgta 120
 |||||
 DB 1322 AGTGCATCTCCAGACAGGCTTATTTTAAAAAGATTGTTTGTCAAGTGTCAATGTGA 1381

QY 121 ggtctgcaccacagggtggtggaatgttctgacagaaggagaagatctagaatgtgt 180
 |||||
 DB 1382 GGTCTGTGACACCCAGGCTGGGGAATGTTTGGCGCAAGAGGAGATCTTGAAATGTCT 1441

QY 181 ttctcgaataacattgt 239
 |||||
 DB 1442 TTCTCGAATAACATTTGT 1500

RESULT 3
 AX331545 3426 bp DNA linear PAT 09-JAN-2002
 LOCUS AX331545
 DEFINITION Sequence 2054 from Patent WO0194629.
 ACCESSION AX331545
 VERSION AX331545.1 GI:18122179
 KEYWORDS human.
 SOURCE Homo sapiens

REFERENCE 1 (sites)
 AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ehner,R., Endress,G.,
 Horrigan,S., Soppet,D.R. and Weaver,Z.
 TITLE Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 2054 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 FEATURES location/Qualifiers
 source 1..3426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 887 a 799 c 920 g 820 t

ORIGIN

Query Match 100.0%; Score 239; DB 6; Length 3426;
 Best Local Similarity 100.0%; Pred. No. 5.1e-62;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctggttcattctactgtagctgacgtatgacacacagtggttgcattggtgacctg 60
 |||||
 DB 1262 CTGTTTCAATTTCTACTGCTGACTGATGTACATCACAGTGTTCGAATGCTGCCCTG 1321

QY 61 agtgcattcccaagaccaggtttttaaaagattgtttgtcgaagtgcatactgta 120
 |||||
 DB 1322 AGTGCATCTCCAGACAGGCTTATTTTAAAAAGATTGTTTGTCAAGTGTCAATGTGA 1381

QY 121 ggtctgcaccacagggtggtggaatgttctgacagaaggagaagatctagaatgtgt 180
 |||||
 DB 1382 GGTCTGTGACACCCAGGCTGGGGAATGTTTGGCGCAAGAGGAGATCTTGAAATGTCT 1441

QY 181 ttctcgaataacattgt 239
 |||||
 DB 1442 TTCTCGAATAACATTTGT 1500

RESULT 4
 HS043653 3426 bp mRNA linear PRI 14-MAR-1996
 LOCUS HS043653
 DEFINITION Human obese protein (ob) mRNA, complete cds.
 ACCESSION U43653
 VERSION U43653.1 GI:1226243
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 3426)
 AUTHORS Gong,D.W., Bl,S., Pratlery,R.E. and Weintrub,B.D.
 TITLE Genomic structure and promoter analysis of the human obese gene
 JOURNAL J. Biol. Chem. 271 (8), 3971-3974 (1996)
 MEDLINE 9623958
 REFERENCE 2 (bases 1 to 3426)
 AUTHORS Gong,D.-W.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-1995) Da-Wei Gong, Molecular and Cellular
 Endocrinology Branch, NIDDK/NIH, Bldg10/RmBld1, 10 Center Drive
 MSC1822, Bethesda, MD 20892, USA
 FEATURES location/Qualifiers
 source 1..3426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"
 1..3426
 /gene="Ob"
 57..560
 /gene="Ob"
 /codon_start=1
 /product="obese protein"
 /protein_id="AAC50400.1"
 /db_xref="GI:1226244"

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/translation="MHNGSTLGGFLMLPYLFYVQAVPIQKVVODTKILIKITIVRIND
ISHQVSISSKOKATYTGDPITPELHPILILSKMDOTLAVYQOILITSMPSRNVIIQSNLDE
NLRLCLHVLAFSKSCHLPWASGLETITDLSGLVLEASGYSTEVALSLRQIDLMQ
LDLSPGC"
BASE COUNT      887 a      799 c      920 g      820 t
ORIGIN

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Query Match	100.0%;	Score 239;	DB 9;	Length 3426;
Best Local Similarity	100.0%;	Pred. No. 5.1e-62;		
Matches 239;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ctggattcattctcaacgctacgacgattacatcaacaggtttgcgaatggtgtccctg	60
Db	1262	CTGGTTTCATTCTTACGTCAGTCAGATTACATCACAGCTTTGCCAATGGTGTCCCTG	1321
Qy	61	agtgatccccaagaccaggtatttttaaaagaatttgctgtcaagtgcatactga	120
Db	1322	AGTGAATCTCCAAAGGACACAGCTATTATTTAAAAAGATTTGTTTGCAGTGTCAATGTA	1381
Qy	121	ggtgtctgcaccccaagggtgtgggaaatgcttgggcgaagagggaagaagatcagaatgtgt	180
Db	1382	GGGTGTGACCCCAAGGGGTGGGAAAGTTTGGGCACAAAGGGAAGGATCTTGAATGTGT	1441
Qy	181	ttctcgataacaatttgtgtgtgtgttcttcggaaagagttagatcaatttcattcat	239
Db	1442	TTTCTGAATTAACATTGTGTGTGTGGGTCTCTTTCGGAAGGATAGATCATTTTCTTAATCT	1500

RESULT	5				
D63708S3					
LOCUS	D63708S3	4522 bp	DNA	linear	PRI 14-APR-2000
DEFINITION	Human cb gene, exon 3 and complete cds.				
ACCESSION	D63710				
VERSION	D63710.1 GI:1071653				
KEYWORDS	Oese, gene; ob protein.				
SOURCE	3 Of 3				
-	Homo sapiens leukocyte DNA, clone_1lb:lambda EMBL3 (CLONETECH)				

ORGANISM	Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	
1 (bases 1 to 4522)	
REFERENCE	Isse, N., Ogawa, Y., Tamura, N., Masuzaki, H., Mori, K., Okazaki, T.,
AUTHORS	

TITLE	Structural organization and chromosomal assignment of the human obese gene
JOURNAL	J. Biol. Chem. 270 (46), 27728-27733 (1995)
MEDLINE	96070903
REFERENCE	2 (bases 1 to 4522)
SEQUENCE	
FEATURES	

TITLE Direct Submission
JOURNAL Submitted (31-JUL-1995) Yoshiohri Ogawa, Kyoto University Graduate School of Medicine, Dept. of Medicine and Clinical Science, 54 Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (tel:075-751-3173, Fax:075-771-9452)

intron

exon

BASE COUNT	1189	a	1032	c	1177	g	1124	t
ORIGIN	/standard_name="obese" /number=3							

Query Match	100.0%	Score 239;	DB 9;	Length 4522;
Best Local Similarity	100.0%;	Pred. No. 5e-62;		
Matches 239;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	ctggatcattccacacgtyacgaagttacatcacaaagtggttgcacg	60
Db	1092	CTGGTTCATTCTTCTACGTGTACTGATGATTACATCACAGCTTTGCCAATGCTTGCCTG	1155
Oy	61	agtygaattccaaagacacgaattattttaaaaaagatttggttcgaagtgcatalgta	120
Db	1152	AGTGGATCTCCAAAGCAGCAGGTTATTTTAAAAAGATTTTCTTTGTCACATGCTCATATGTA	1211
Oy	121	ggtgtctcgaccccaagggtgagggaatgcttggtgcagaaggaaggaagatcctagaatggt	180
Db	1212	GGGTCTGCGACACCAGGGGTGGGGAATGTTTGGGCAAAAGGAGAACTGTAATGTGT	1271
Oy	181	ttcttgaaataacatttgggtggtggtctcttggaagaggtagatcatcttcttatct	239
Db	1272	TTTCTGATATACATTTGTGTGGTGGGTTCTTTTGCAAGAGGTAGATCATTTTCTTATCT	1330

RESULT	6
G31731	4522 bp DNA linear STS 28-SEP-1998
LOCUS	SWS2619 Eric D. Green Homo sapiens STS genomic, sequence tagged
DEFINITION	
ACCESSION	G31731
VERSION	G31731.1 GI:1916456
KEYWORDS	STS.
SOURCE	human.
ORIGIN	

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 4522)	Bouffard, G. G., Iyer, L. M., Idol, J. R., Braden, V. V., Cunningham, Weintraub, L. A., Mohr-Tidwell, R. M., Peluso, D. C., Fulton, R. S., Leckie, M. P. and Green, E. D.	A collection of 1814 human chromosome 7-specific STSS	Genome Res. 7 (1), 59-64 (1997)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2 (bases 1 to 4522)	Green, E.D.	Human chromosome 7 STS (1997)	Unpublished	Synonyms: 085

National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CGTTAAGGGAAGCAACTCTCG

National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CGTTAAGGGAAGCAACTCTCG

National Human Genome Research Institute/NIH
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Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CGTTAAGGGAAGCAACTCTCG

National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CGTTAAGGGAAGCAACTCTCG

Primer B: TGGCTTAGAGAGTCAGGCA
STS size: 106
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 50 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600

Protocol:

Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:

MgCl2: 1.5 mM
KCl: 100 mM
Tris-HCl: 10 mM
NH4Cl: 5 mM
pH: 8.6

This STS has been incorporated into the NHGRI chromosome 7 physical map, but was developed by another investigator. See Genbank record: D63710 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID-92128937].

FEATURES

Source
1..4522
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="7"
/clone_lib="Eric D. Green"
1..4522
/gene="OBS"
423..528
/gene="OBS"
423..443
/gene="OBS"
primer_bind complement(509..528)
primer_bind 1189 a 1032 c 1177 g 1124 t
BASE COUNT 1189 a 1032 c 1177 g 1124 t
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 239; DB 11; Length 4522;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ctggttcattcttactgtactgactgattacacacagtgttgcgaatggttcctg 60
1092 ctggttcttactgtactgactgactgactgactgactgactgactgactg 1151
QY 61 agtgaatcccaagcaggttatttaaaagaattgttgcgaatgactatgta 120
Db 1152 agtgaatcccaagcaggttatttaaaagaattgttgcgaatgactatgta 1211
QY 121 ggtgtcgtgacccaggggtggaatggttggcagaaggaaggaatctagaatgtg 180
Db 1212 ggtgtcgtgacccaggggtggaatggttggcagaaggaaggaatctagaatgtg 1271
QY 181 ttctgataacaattgtgtggtggttcttggaaaggaatgagatcttctatct 239
Db 1272 ttctgataacaattgtgtggtggttcttggaaaggaatgagatcttctatct 1330

RESULT

AC018635 163549 bp DNA linear PRT 15-NOV-2001
LOCUS Homo sapiens chromosome 7 clone RP11-62J1, complete sequence.
AC018635
AC018635 7 GI:16930995

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 163549)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C., and

Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 163549)

Bubb, K.L., Desmarais, C.L., Ramsey, S.A. and Hubley, R.M.

Direct Submission

Submitted (15-DEC-1999) Human Genome Center, University of

Washington, Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 163549)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C.,

Clendenning, J., Ivey, R.G. and Haugen, E.D.

Direct Submission

Submitted (31-MAR-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

4 (bases 1 to 163549)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C. and

Haugen, E.D.

Direct Submission

Submitted (15-NOV-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

On Nov 15, 2001 this sequence version replaced gi:13491250.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu

----- Project Information

Center project name: chr-7

Center clone name: RP11-62J1 (djs169)

----- Summary Statistics

Assembly program: Phrap; version 0.990319

Consensus quality: 163396 bases at least Q40

Consensus quality: 163533 bases at least Q30

Consensus quality: 163548 bases at least Q20

Insert size: 177112; 11.9% error; agarose-tp

Insert size: 163539; sum-of-contigs

Quality coverage: 9.0x in Q20 bases; agarose-tp

Quality coverage: 9.7x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': RP11-339C9 (UWGC:djs166) AC018662 20141-bp clone overlap

3': RP11-155G14 (UWGC:djs356) AC010655 54910-bp clone overlap

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

Genbank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an

alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest

fingerprinting. Comparison of the experimentally derived digest

fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and

COMMENT	OS	Canis sp. (dog)
	PN	JP 2000279171-A/18
	PD	10-OCT-2000
	PF	30-MAR-1999 JP 1999088295
	PR	
	PI	TSUNOMU HONSHO, MASAYUKI, SAIRO
	PC	C12N15/09, C07K14/47, C07K16/18, C12N1/21, C12P21/02, G01N33/53//
	PC	(C12P21/02, C12R1:19), C12N15/00
	CC	
	FC	
	FT	
	FT	
FEATURES	source	Location/Qualifiers 1..2925 /organism="Canis sp." /db_xref="taxon:9616"
BASE COUNT	742 a	707 c 766 g 710 t
ORIGIN		
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Best Local Similarity	78.7%:	Pred. NO. 6.5e-29;
Matches 181:	Conservative 0;	Mismatches 45; Indels 2;
QY	1	ctggttcattcttctactgactgagtgatcatcacacagtgatttgcgaatggtgtgcctg 60
Db	1123	CTGGCTATGTTTCTTCTACTGTGACGAGTGAATATACATGTTTGCATGCAATGCCATGCCCTG 1182
QY	61	agtgatattccaaaggaccaggtattttaa---aagatttgattgtcgaatgcatcat 117
Db	1183	AGCGGATCTCCAGAGACACAGGATTATTTGAAAAAGAAATGAATTTTGTCATGTGTGATAT 1242
QY	118	gtagggtctcaccacccagggt-ggggaagattttgggagaaggagaagatctagaat 176
Db	1243	ATAGATGTGTGTACTCTGACGAGTAGGAGAACGCTGTTATGACGAGAAAGGCGAAGATCCAGAT 1302
QY	177	gtgtttctgaataacatttgytgytggtctcttggaaagatgagat 226
Db	1303	GTATTTTGAATTTACATTTGTGCGATGGCGCTTCGAATGAGAGGGGGGT 1352
RESULT 12		
LOCUS	ARI175617	2793 bp DNA linear PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6309853.	
ACCESSION	ARI175617	
VERSION	ARI175617.1	GI:17916916
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 2793)	
AUTHORS	Friedman,J.M., Zhang,Y. and Proenca,R.	
TITLE	Modulators of body weight, corresponding nucleic acids and	
JOURNAL	proteins, and diagnostic and therapeutic uses thereof	
FEATURES	Patent: US 6309853-A 1 30-OCT-2001;	
SOURCE	Location/Qualifiers 1..2793 /organism="unknown"	
BASE COUNT	689 a	653 c 740 g 711 t
ORIGIN		
Query Match	33.7%:	Score 80.6; DB 6; Length 2793;
Best Local Similarity	65.4%:	Pred. NO. 6.6e-14;
Matches 151:	Conservative 0;	Mismatches 74; Indels 6; Gaps 2;
QY	1	ctggttcattcttctactgactgagtgatcatcacacagtgatttgcgaatggtgtgcctg 60
Db	1225	CTGGTTTGTGTTCTATTTGTGACTGACTATACCAAAACAGTTTGACAGGCGCATTTGCC--- 1281
QY	61	agtgatctccaaaggaccaggtattttaaanaagattgttttgcgaatgcatatgta 120

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Db 1282 --GGGACATAGGCTAGTATTATATCAAAAGCATGATTTTGTCAAGTGTATATGTA 1339
Qy 121 ggtgtctgaccccaagggtgttggaatgttggcagaaggaaggaatagatgtgt 180
Db 1340 TCTATGTGACCTGAGGAGTATGCTGTAGAGGAGGAGGATCCGGA-CTGT 1398
Qy 181 ttctgaataacatttgtgtgtgtgttcttggaaaggaatgagatcatt 231
Db 1399 TCTCTGAATTACATATGTGTGTAGGCTTTTCTGAAAGGCTAGGCAATTTT 1449

RESULT 13
AX088104 2793 bp DNA linear PAT 17-MAR-2001
LOCUS AX088104
DEFINITION Sequence 1 from Patent WO0113935.
ACCESSION AX088104
VERSION AX088104.1 GI:13397026
KEYWORDS
SOURCE Murinae gen. sp.
ORGANISM Murinae gen. sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE 1 (bases 1 to 2793)
AUTHORS Banks, W.A.
TITLE Modulation of the blood-brain barrier transporter for leptin
JOURNAL Patent: WO 0113935-A 1 01-MAR-2001;
Tulane University (US)
FEATURES
source 1..2793
/organism="Murinae gen. sp."
/db_xref="taxon:39108"
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CDS 57..560
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/codon_start=1
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ISHTQSVAKORVGTGLDPIGRIPLISLMDQTLAVYQOVLSPSONVLOIANLE
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ORIGIN
Query Match 33.7%; Score 80.6; DB 6; Length 2793;
Best Local Similarity 65.4%; Pred. No. 6.6e-14;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

Qy 1 ctggttcatttctactgtgactgtatcatcacagtggttgcaatgtgtgacctg 60
Db 1225 CTGGTTTGTGTTCTATTGTGACTGACTATCCAAACACCTTTCAGCGCATTTGCC--- 1281
Qy 61 agtgcattcccaaggaagcaggattttaaagaagattgttgcgaagtcatatgta 120
Db 1282 --GGGACATAGGCTAGGCTATTATATCAAAAGCATGATTTTGTCAAGTGTATATGTA 1339
Qy 121 ggtgtctgaccccaagggtgttggaatgttggcagaaggaaggaatagatgtgt 180
Db 1340 TCTATGTGACCTGAGGAGTATGCTGTAGAGGAGGAGGATCCGGA-CTGT 1398
Qy 181 ttctgaataacatttgtgtgtgtgttcttggaaaggaatgagatcatt 231
Db 1399 TCTCTGAATTACATATGTGTGTAGGCTTTTCTGAAAGGCTAGGCAATTTT 1449

RESULT 14
MMU18812 2793 bp mRNA linear ROD 30-MAR-1995
LOCUS MMU18812
DEFINITION Mus musculus obese precursor (ob) mRNA, complete cds.

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```

ACCESSION U18812
VERSION U18812.1 GI:746416
KEYWORDS mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2793)
AUTHORS Zhang, Y., Proenca, R., Maffei, M., Barone, M., Leopold, L. and
Friedman, J.M.
TITLE Positional cloning of the mouse obese gene and its human homologue
JOURNAL Nature 372 (6505), 425-432 (1994)
MEDLINE 95075453
REFERENCE 2 (bases 1 to 2793)
AUTHORS Friedman, J.M.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-1994) Jeffrey M. Friedman, Howard Hughes Medical
Institute, The Rockefeller University, P.O. Box 305, 1230 York
Ave., New York, NY 10021, USA
On Mar 30, 1995 this sequence version replaced gi:603287.
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/chromosome="6"
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LDVSPC"
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/feature="putative"
120..557
/gene="ob"
/standard_name="obese"
/product="unnamed"
BASE COUNT 689 a 653 c 740 g 711 t
ORIGIN
Query Match 33.7%; Score 80.6; DB 10; Length 2793;
Best Local Similarity 65.4%; Pred. No. 6.6e-14;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

Qy 1 ctggttcatttctactgtgactgtatcatcacagtggttgcaatgtgtgacctg 60
Db 1225 CTGGTTTGTGTTCTATTGTGACTGACTATCCAAACACCTTTCAGCGCATTTGCC--- 1281
Qy 61 agtgcattcccaaggaagcaggattttaaagaagattgttgcgaagtcatatgta 120
Db 1282 --GGGACATAGGCTAGGCTATTATATCAAAAGCATGATTTTGTCAAGTGTATATGTA 1339
Qy 121 ggtgtctgaccccaagggtgttggaatgttggcagaaggaaggaatagatgtgt 180
Db 1340 TCTATGTGACCTGAGGAGTATGCTGTAGAGGAGGAGGATCCGGA-CTGT 1398
Qy 181 ttctgaataacatttgtgtgtgtgttcttggaaaggaatgagatcatt 231
Db 1399 TCTCTGAATTACATATGTGTGTAGGCTTTTCTGAAAGGCTAGGCAATTTT 1449

RESULT 15
AC072048/c 214257 bp DNA linear HTG 15-NOV-2001
LOCUS AC072048

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DEFINITION Mus musculus chromosome 6 clone RP23-169E15 strain C57BL6/J,
WORKING DRAFT SEQUENCE, 14 unordered pieces.
AC072048
VERSION AC072048.2 GI:16930942
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 214257)
AUTHORS Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Binkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Lalic, P., Lee-Lin, S.-O.,
Legaspi, R., Maduro, O.L., Maduro, V.B., Masicilo, C., Mastrian, S.D.,
McCluskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,
Stancirpop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 214257)
Green, E.D.
Direct Submission
Submitted (07-JUN-2000) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
On Nov 15, 2001 this sequence version replaced gi:8313202.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@nhgri.nih.gov
----- Project Information
Center project name: wp
Center clone name: 169E15
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 206853 bases at least Q40
Consensus quality: 207842 bases at least Q30
Consensus quality: 208446 bases at least Q20
Insert size: 209000; agarose-fp
Insert size: 197000; pulse-field-gel
Insert size: 212957; sum-of-coverage
Quality coverage: 11.38x in Q20 bases; agarose-fp
Quality coverage: 12.07x in Q20 bases; pulse-field-gel
Quality coverage: 11.17x in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 6798: contig of 6798 bp in length
* 6799 6898: gap of unknown length
* 6899 15014: contig of 8116 bp in length
* 15015 15114: gap of unknown length
* 15115 24240: contig of 9126 bp in length
* 24241 24340: gap of unknown length
* 24341 32924: contig of 8584 bp in length
* 32925 33024: gap of unknown length
* 33025 44801: contig of 11777 bp in length
* 44802 44901: gap of unknown length
* 44902 55618: contig of 10717 bp in length
* 55619 55719: gap of unknown length
* 55720 69004: contig of 13286 bp in length
* 69005 69104: gap of unknown length
* 69105 82272: contig of 13168 bp in length
* 82273 82372: gap of unknown length

FEATURES
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/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="6"
/clone="RP23-169E15"
/clone_1ib="RPC1 mouse BAC library 23"
1..6798
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6899..15014
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15115..24240
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24341..32924
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69105..82272
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82373..99277
/note="assembly-fragment"
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misc_feature
149220..175493
/note="assembly-fragment"
misc_feature
175594..214257
/note="assembly-fragment"
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BASE COUNT 55999 a 50290 c 50579 g 56076 t 1313 others
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Best Local Similarity 65.4%; Pred. No. 4.6e-14;
Matches 151; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
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QY 1 ctggttctattctactgtctacgtatgtatcatcacagctgttctcatatgtgtccctg 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 183716 CTGGTTTGTGTTTATGTCAGCTATGCAACACGTTTCCACGGCATTGCC-- 183658
*
QY 61 agtggatctcccaaggccaggtatatttcaaaagattgttttcaagtgcatactgta 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 183659 --GGGACATAGGCTAGGTATATATCAAAAGCAGATCAATTTTGTCAAGTATATGTA 183602
*
QY 121 ggtgtctgaccaccaggagtggtgggaattgttggcagaagaaggagaagatctagaatg 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 183601 TGTATCTGCACCTGAGAGGTAGAGATGTGTAGAGGAGGAGGATCGGAA--GTGT 183543
*
QY 181 ttctgataacaattgtgtgtgtgtcttcttgaagagatgagatcatc 231
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 183542 TCTCTGATATACATATGTGTGTAGGCTTTCTGAAAGGCGTGAAGCATTTT 183492

Search completed: June 13, 2002, 15:50:57
Job time: 10869 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:43 ; Search time 1785.18 Seconds
(without alignments)
1806.973 Million cell updates/sec

Title: US-09-437-458-17

Perfect score: 239
Sequence: 1 ctggttcattctctactgty.....gtgagatcattctctatct 239

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST : *

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40.4	16.9	465	12	AQ004645 C1T-HSP-2
C 2	39.2	16.4	1050	12	CNS013NS AL103090 Drosophila
C 3	39.2	16.4	1101	12	CNS013NS AL107874 Drosophila
C 4	38.4	16.1	1201	12	CNS016HY AL106552 Drosophila
C 5	36.4	15.2	884	12	CNS006U0 AL065923 Drosophila
C 6	36.4	15.2	1201	12	CNS016Z2 AL106227 Drosophila
C 7	36.2	15.1	341	10	BE322138 NF010E031
C 8	35.6	14.9	621	10	BM121183 L0949E03-
C 9	35.6	14.9	848	12	CNS006W0 AL072642 Drosophila
C 10	35.6	14.9	1101	12	CNS000D1 AL065414 Drosophila
C 11	35.6	14.9	1101	12	CNS000Z0 AL097326 Drosophila
C 12	35.4	14.8	376	12	AQ260214 C1TBI-EI-
C 13	35.4	14.8	637	12	AZ589172 IM0398A06
C 14	35.2	14.7	897	12	CNS015FK AL105386 Drosophila
C 15	34.8	14.6	859	10	CNS004YV AL055406 Drosophila
C 16	34.6	14.5	791	10	BG474557 BG02517334
C 17	34.4	14.4	621	12	AZ235467 RPCI-23-6

C 18	34.4	14.4	1101	12	CNS016JY AL106840 Drosophila
C 19	34.2	14.3	939	12	CNS00CNG AL059400 Drosophila
C 20	34.2	14.3	1101	12	CNS0039G AL063921 Drosophila
C 21	34	14.2	436	10	BF408218 BF408218 UI-R-BJ2-
C 22	34	14.2	633	10	BM390047 BM390047 UI-R-CN1-
C 23	33.8	14.1	316	9	BA490430 BA490430
C 24	33.8	14.1	328	9	AA668450 AA668450.s
C 25	33.8	14.1	328	9	AA668454 ab86405.s
C 26	33.8	14.1	522	10	BM343932 BM343932 r144903.Y
C 27	33.8	14.1	877	12	AQ867363 AQ867363 nbebd00310
C 28	33.8	14.1	882	12	AZ686073 AZ686073 ENTME14TR
C 29	33.8	14.1	895	12	CNS0071A AL066286 Drosophila
C 30	33.8	14.1	904	12	AZ550922 A2550922 ENTF190TR
C 31	33.8	14.1	1127	12	CNS01XMK AL172253 Tetradon
C 32	33.6	14.1	500	9	AU086071 AU086071
C 33	33.6	14.1	712	12	AZ382973 AZ382973 1M0140P03
C 34	33.4	14.0	411	10	BG304410 BG304410 F186H02.Y
C 35	33.4	14.0	453	9	AU006663 AU006663
C 36	33.4	14.0	743	12	CNS0406F AL268512 Tetradon
C 37	33.4	14.0	793	12	CNS043S0 AL273177 Tetradon
C 38	33.4	14.0	924	10	BG336429 BG336429
C 39	33.2	13.9	318	9	AV163550 AV163550
C 40	33.2	13.9	693	9	BB358710 BB358710
C 41	33.2	13.9	840	12	BH165678 BH165678 ENTYS02TF
C 42	33.2	13.9	859	12	CNS00KLL AL077728 Drosophila
C 43	33.2	13.9	924	12	BH150220 BH150220 ENTF195TR
C 44	33.2	13.9	967	12	CNS00K7Z AL078030 Drosophila
C 45	33.2	13.9	1003	12	AG076031 AG076031 Pan trogl

ALIGNMENTS

RESULT 1
LOCUS AQ004645/c 465 bp DNA linear GSS 26-JUN-1998
DEFINITION C1T-HSP-2127C7.FP C1T-HSP Homo sapiens genomic clone 2127C7, DNA sequence.
ACCESSION AQ004645
VERSION AQ004645.1 GI:3081100
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 465)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden K., Berry,K., Granger,D., Suh,E., Wible,C., Kim,U.-J., Shizuya,H., Simon,M. and Venter,J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
FEATURES
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/clone="2127C7"
/clone_lib="C1T-HSP"
/sex="Male"
/cell_type="Sperm"


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/note="Vector: pBelobAC11, Site_1: HindIII, Site_2: HindIII"
BASE COUNT      129 a      125 c      69 g      142 t
ORIGIN

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Best Local Similarity 51.1%; Pred. No. 0.61;
Matches 95; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 47 atggtgttcctcagtgatcctcaagaccagatatttaaaagattgttctg 106
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Db 437 AAGAGAGAGCGCTTCATGCTGACACAGCAAGAAAGAAATTCAGAAAAGCTTCCTTT 378

Qy 107 aagtgatcatgttagtgcctcaccacccaggggtgggaattgttgcgaagaaggagaag 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 GGGTGTGCTTAAATTAATCTACTCTCACTGTTTGGGAGACATCAGTCATACATG 318

Qy 167 gatcagaatgtgttctcgaataacattgtgtgtgtgtgttcttggaaagatgagat 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    317 GCTCGTAATACCTTTGCTGCTTCATGATGCTGCTGGGAGCTTGAAGAGGTTGAGAT 258

vY 227 catctt 232
    |||
Db 257 CTATAT 252

RESULT 2
LOCUS      CNS013NS      1050 bp      DNA      linear      GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN10C02 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL103090
VERSION     AL103090.1 GI:5614701
KEYWORDS   GSS.
SOURCE      fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1050)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (BDGP) -
            http://www.edgp.edi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelobAC11.

FEATURES
    source      Location/Qualifiers
                1..1050
                /organism="Drosophila melanogaster"
                /plasmid="pBelobAC11"
                /db_xref="taxon:7227"
                /clone_lib="DrosBAC"
                /clone="BACN10C02"
                /note="end : SP6"
BASE COUNT      308 a      203 c      14 g      328 t      197 others
ORIGIN

Query Match      16.4%; Score 39.2; DB 12; Length 1050;
Best Local Similarity 36.5%; Pred. No. 1.5;
Matches 65; Conservative 36; Mismatches 77; Indels 0; Gaps 0;

Qy 60 gaatgatcccaagaccgggtattttaaaagattgttgcgaagtgcatatgt 119
    ||| ||| : : : : : ||||| : : : : : ||| : : : : : ||| : : : : :

```

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Db 644 GCGKAGAGCKTKRATKAGCTTAAATTGGCTKCTTKKKGCAATAATKATKAT 585

Qy 120 aggtgtctgcaccacaggggtgggaatgttltggcagaaggagaagatcagaatgtg 179
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 584 TGATCMGSMGMAKMAKKAGAGGSGKCGAKTBKAKGCGGGGCGKAGKAGTKKGTG 525

Qy 180 ttcttgataacattgtgtgtgtgtgttcttggaaagatgagatcatttctat 237
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 524 GAARMAAATGMAATTKTKTGTCGCAAWTTGGADGARAATAATWATTTTWT 467

RESULT 3
LOCUS      CNS00LT2      1101 bp      DNA      linear      GSS 14-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR48P19 of RPCT-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL078714
VERSION     AL078714.1 GI:5102004
KEYWORDS   GSS.
SOURCE      fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazuhiro Oseogawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCT-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bdgpc.med.buffalo.edu/drosophila_bac.htm.

FEATURES
    source      Location/Qualifiers
                1..1101
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="RPCT-98"
                /clone="BACR48P19"
                /note="end : TET3"
BASE COUNT      469 a      6 c      69 g      151 t      406 others
ORIGIN

Query Match      16.4%; Score 39.2; DB 12; Length 1101;
Best Local Similarity 22.3%; Pred. No. 1.5;
Matches 49; Conservative 82; Mismatches 89; Indels 0; Gaps 0;

Qy 5 ttcatctctactgtactgattacacagatgttgcgaatgtgttgcctcagtg 64
    ||| ||| : : : : : ||| ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 651 TTTTATTAKTKTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 710

Qy 65 gatctcaagaccaggtattttaaaagattgttgcgaatgtgcataatgagtg 124
    : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 711 DKWDAKRWDAKATKTKTKDKKAAAMADKKDKKGGKGGKGGKGGKGGKGGKGGK 770

Qy 125 tctgaccacaggggtgggaatgttltggcagaaggagaagatcagaatgttctc 184
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 771 GKGGMGKGGKKAADDKDKTKKKKKAATTTTTKKKKGGKGGKGGKGGKKAADTKTK 830

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Oy 99 gttctgtccaanlytgcatactgtagtgyltcgcagccagggytggggaatgltttggcgcaaa 150
 Db 250 ATGTAATTACCTATATTATTCATGTATTTTGAGACATATGGTTTTCTTATATGCTCATGAGAC 191
 Oy 159 ggagagaagacctaagaatgltttcttcogaataacaatttgttgt 203


```

RESULT 15
CNS004YY/C
LOCUS
DEFINITION CNS004YY 859 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TEf3 end of BAC #
BACR11F03 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL055406
VERSION AL055406.1 GI:4932207
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Source
1. 859
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11F03"
/note="end : TEf3"
BASE COUNT 302 a 32 c 15 g 124 t 386 others
ORIGIN
Query Match 14.6%; Score 34.8; DB 12; Length 859;
Best Local Similarity 13.9%; Pred. No. 24;
Matches 25; Conservative 91; Mismatches 64; Indels 0; Gaps 0;
vY 46 aatggtgtgcctgagtcgacatccaaagcagcaggtatttaaaagtgtgtgt 105
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 816 RRTDRTTTRRRRTTTRRRRTTTRRRRTTTRRRRTTTRRRRTTTRRRRTTTR 757
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 106 caagtgtcatatgtagtctgcaccaggggtgggaaatgttggcagaaggagaa 165
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 756 WRRRTTTRTTRRRRTTTRTTRRRRTTTRRRRTTTRRRRTTTRRRRTTTR 697
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 166 ggaatcagaatgtgttctgaataacattgtgtgtgtgtgtgtgtgtgtgaga 225
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 696 DRDWDTRRRRRCCTTRRRRDARRRRDRTTGDRRTTDTTRTARTTRARRRRGRKR 637
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Search completed: June 13, 2002, 15:17:37
Job time: 8874 sec